



SEQUENCE LISTING

<110> Rieping, Mechthild
Farwick, Mike

<120> Process for the production of L-amino acids using strains of the
Enterobacteriaceae family

<130> 7909/84003

<140> US/10/817,431

<141> 2004-04-05

<160> 8

<170> PatentIn version 3.1

<210> 1
<211> 30
<212> DNA
<213> Artificial
<220>
<223> PCR Primer

<220>
<221> Restriction site
<222> (9)..(14)
<223> XbaI site

<400> 1
gaacaaatct agaaattaag ccgggggaggc 30

<210> 2
<211> 24
<212> DNA
<213> Artificial
<220>
<223> PCR Primer

<220>
<221> Restriction site
<222> (8)..(13)
<223> HindIII site

<400> 2
gctacttaag ctttacaggc tttc 24

<210> 3
<211> 431
<212> DNA
<213> Escherichia coli
<220>
<221> yfiD PCR product
<222> (1)..(431)
<223>

<220>
<221> CDS

```
<222> (36)..(419)
<223> open reading frame yfiD
```

[illegible]

```
<210> 4
<211> 127
<212> PRT
<213> Escherichia coli
```

<400>	4														
Met	Ile	Thr	Gly	Ile	Gln	Ile	Thr	Lys	Ala	Ala	Asn	Asp	Asp	Leu	Leu
1				5					10					15	
Asn	Ser	Phe	Trp	Leu	Leu	Asp	Ser	Glu	Lys	Gly	Glu	Ala	Arg	Cys	Ile
			20					25					30		
Val	Ala	Lys	Ala	Gly	Tyr	Ala	Glu	Asp	Glu	Val	Val	Ala	Val	Ser	Lys
		35					40					45			
Leu	Gly	Asp	Ile	Glu	Tyr	Arg	Glu	Val	Pro	Val	Glu	Val	Lys	Pro	Glu
	50					55					60				
Val	Arg	Val	Glu	Gly	Gly	Gln	His	Leu	Asn	Val	Asn	Val	Leu	Arg	Arg
65					70					75					80
Glu	Thr	Leu	Glu	Asp	Ala	Val	Lys	His	Pro	Glu	Lys	Tyr	Pro	Gln	Leu
				85					90					95	

Thr Ile Arg Val Ser Gly Tyr Ala Val Arg Phe Asn Ser Leu Thr Pro
 100 105 110

Glu Gln Gln Arg Asp Val Ile Ala Arg Thr Phe Thr Glu Ser Leu
 115 120 125

<210> 5
 <211> 28
 <212> DNA
 <213> Artificial
 <220>
 <223> PCR Primer

<220>
 <221> Restriction site
 <222> (5)..(10)
 <223> XbaI site

<400> 5
 ccactctaga aggtaggtgt tacatgtc

28

<210> 6
 <211> 27
 <212> DNA
 <213> Artificial
 <220>
 <223> PCR Primer

<220>
 <221> Restriction site
 <222> (13)..(18)
 <223> HindIII site

<400> 6
 cgatttcagt caaagcttat tacatag

27

<210> 7
 <211> 2325
 <212> DNA
 <213> Escherichia coli

<220>
 <221> pflB PCR product
 <222> (1)..(2325)
 <223>

<220>
 <221> CDS
 <222> (24)..(2306)
 <223> pflB coding region

<400> 7
 ccactctaga aggtaggtgt tac atg tcc gag ctt aat gaa aag tta gcc aca
 Met Ser Glu Leu Asn Glu Lys Leu Ala Thr
 1 5 10

53

gcc tgg gaa ggt ttt acc aaa ggt gac tgg cag aat gaa gta aac gtc
 Ala Trp Glu Gly Phe Thr Lys Gly Asp Trp Gln Asn Glu Val Asn Val
 15 20 25

101

cgt	gac	ttc	att	cag	aaa	aac	tac	act	ccg	tac	gag	ggt	gac	gag	tcc	149
Arg	Asp	Phe	Ile	Gln	Lys	Asn	Tyr	Thr	Pro	Tyr	Glu	Gly	Asp	Glu	Ser	
			30					35					40			
ttc	ctg	gct	ggc	gct	act	gaa	gcg	acc	acc	acc	ctg	tgg	gac	aaa	gta	197
Phe	Leu	Ala	Gly	Ala	Thr	Glu	Ala	Thr	Thr	Thr	Leu	Trp	Asp	Lys	Val	
		45					50					55				
atg	gaa	ggc	gtt	aaa	ctg	gaa	aac	cgc	act	cac	gcg	cca	ggt	gac	ttt	245
Met	Glu	Gly	Val	Lys	Leu	Glu	Asn	Arg	Thr	His	Ala	Pro	Val	Asp	Phe	
	60					65					70					
gac	acc	gct	gtt	gct	tcc	acc	atc	acc	tct	cac	gac	gct	ggc	tac	atc	293
Asp	Thr	Ala	Val	Ala	Ser	Thr	Ile	Thr	Ser	His	Asp	Ala	Gly	Tyr	Ile	
75					80					85					90	
aac	aag	cag	ctt	gag	aaa	atc	gtt	ggt	ctg	cag	act	gaa	gct	ccg	ctg	341
Asn	Lys	Gln	Leu	Glu	Lys	Ile	Val	Gly	Leu	Gln	Thr	Glu	Ala	Pro	Leu	
			95					100						105		
aaa	cgt	gct	ctt	atc	ccg	ttc	ggt	ggt	atc	aaa	atg	atc	gaa	ggt	tcc	389
Lys	Arg	Ala	Leu	Ile	Pro	Phe	Gly	Gly	Ile	Lys	Met	Ile	Glu	Gly	Ser	
			110					115					120			
tgc	aaa	gcg	tac	aac	cgc	gaa	ctg	gat	ccg	atg	atc	aaa	aaa	atc	ttc	437
Cys	Lys	Ala	Tyr	Asn	Arg	Glu	Leu	Asp	Pro	Met	Ile	Lys	Lys	Ile	Phe	
		125					130					135				
act	gaa	tac	cgt	aaa	act	cac	aac	cag	ggc	gtg	ttc	gac	ggt	tac	act	485
Thr	Glu	Tyr	Arg	Lys	Thr	His	Asn	Gln	Gly	Val	Phe	Asp	Val	Tyr	Thr	
	140					145					150					
ccg	gac	atc	ctg	cgt	tgc	cgt	aaa	tct	ggt	gtt	ctg	acc	ggt	ctg	cca	533
Pro	Asp	Ile	Leu	Arg	Cys	Arg	Lys	Ser	Gly	Val	Leu	Thr	Gly	Leu	Pro	
155					160					165					170	
gat	gca	tat	ggc	cgt	ggc	cgt	atc	atc	ggt	gac	tac	cgt	cgc	gtt	gcg	581
Asp	Ala	Tyr	Gly	Arg	Gly	Arg	Ile	Ile	Gly	Asp	Tyr	Arg	Arg	Val	Ala	
				175					180					185		
ctg	tac	ggt	atc	gac	tac	ctg	atg	aaa	gac	aaa	ctg	gca	cag	ttc	act	629
Leu	Tyr	Gly	Ile	Asp	Tyr	Leu	Met	Lys	Asp	Lys	Leu	Ala	Gln	Phe	Thr	
			190					195					200			
tct	ctg	cag	gct	gat	ctg	gaa	aac	ggc	gta	aac	ctg	gaa	cag	act	atc	677
Ser	Leu	Gln	Ala	Asp	Leu	Glu	Asn	Gly	Val	Asn	Leu	Glu	Gln	Thr	Ile	
		205					210					215				
cgt	ctg	cgc	gaa	gaa	atc	gct	gaa	cag	cac	cgc	gct	ctg	ggt	cag	atg	725
Arg	Leu	Arg	Glu	Glu	Ile	Ala	Glu	Gln	His	Arg	Ala	Leu	Gly	Gln	Met	
	220					225					230					
aaa	gaa	atg	gct	gcg	aaa	tac	ggc	tac	gac	atc	tct	ggt	ccg	gct	acc	773
Lys	Glu	Met	Ala	Ala	Lys	Tyr	Gly	Tyr	Asp	Ile	Ser	Gly	Pro	Ala	Thr	
235					240					245					250	
aac	gct	cag	gaa	gct	atc	cag	tgg	act	tac	ttc	ggc	tac	ctg	gct	gct	821
Asn	Ala	Gln	Glu	Ala	Ile	Gln	Trp	Thr	Tyr	Phe	Gly	Tyr	Leu	Ala	Ala	
				255					260					265		
gtt	aag	tct	cag	aac	ggg	gct	gca	atg	tcc	ttc	ggg	cgt	acc	tcc	acc	869
Val	Lys	Ser	Gln	Asn	Gly	Ala	Ala	Met	Ser	Phe	Gly	Arg	Thr	Ser	Thr	
			270					275					280			

ttc	ctg	gat	gtg	tac	atc	gaa	cgt	gac	ctg	aaa	gct	ggc	aag	atc	acc	917
Phe	Leu	Asp	Val	Tyr	Ile	Glu	Arg	Asp	Leu	Lys	Ala	Gly	Lys	Ile	Thr	
		285					290					295				
gaa	caa	gaa	gcg	cag	gaa	atg	gtt	gac	cac	ctg	gtc	atg	aaa	ctg	cgt	965
Glu	Gln	Glu	Ala	Gln	Glu	Met	Val	Asp	His	Leu	Val	Met	Lys	Leu	Arg	
	300					305					310					
atg	gtt	cgc	ttc	ctg	cgt	act	ccg	gaa	tac	gat	gaa	ctg	ttc	tct	ggc	1013
Met	Val	Arg	Phe	Leu	Arg	Thr	Pro	Glu	Tyr	Asp	Glu	Leu	Phe	Ser	Gly	
315					320					325					330	
gac	ccg	atc	tgg	gca	acc	gaa	tct	atc	ggc	ggc	atg	ggc	ctc	gac	ggc	1061
Asp	Pro	Ile	Trp	Ala	Thr	Glu	Ser	Ile	Gly	Gly	Met	Gly	Leu	Asp	Gly	
				335					340					345		
cgt	acc	ctg	gtt	acc	aaa	aac	agc	ttc	cgt	ttc	ctg	aac	acc	ctg	tac	1109
Arg	Thr	Leu	Val	Thr	Lys	Asn	Ser	Phe	Arg	Phe	Leu	Asn	Thr	Leu	Tyr	
			350					355					360			
acc	atg	ggc	ccg	tct	ccg	gaa	ccg	aac	atg	acc	att	ctg	tgg	tct	gaa	1157
Thr	Met	Gly	Pro	Ser	Pro	Glu	Pro	Asn	Met	Thr	Ile	Leu	Trp	Ser	Glu	
		365					370					375				
aaa	ctg	ccg	ctg	aac	ttc	aag	aaa	ttc	gcc	gct	aaa	gtg	tcc	atc	gac	1205
Lys	Leu	Pro	Leu	Asn	Phe	Lys	Lys	Phe	Ala	Ala	Lys	Val	Ser	Ile	Asp	
	380					385					390					
acc	tct	tct	ctg	cag	tat	gag	aac	gat	gac	ctg	atg	cgt	ccg	gac	ttc	1253
Thr	Ser	Ser	Leu	Gln	Tyr	Glu	Asn	Asp	Asp	Leu	Met	Arg	Pro	Asp	Phe	
395				400						405					410	
aac	aac	gat	gac	tac	gct	att	gct	tgc	tgc	gta	agc	ccg	atg	atc	gtt	1301
Asn	Asn	Asp	Asp	Tyr	Ala	Ile	Ala	Cys	Cys	Val	Ser	Pro	Met	Ile	Val	
				415					420					425		
ggc	aaa	caa	atg	cag	ttc	ttc	ggc	gcg	cgt	gca	aac	ctg	gcg	aaa	acc	1349
Gly	Lys	Gln	Met	Gln	Phe	Phe	Gly	Ala	Arg	Ala	Asn	Leu	Ala	Lys	Thr	
			430					435					440			
atg	ctg	tac	gca	atc	aac	ggc	ggc	gtt	gac	gaa	aaa	ctg	aaa	atg	cag	1397
Met	Leu	Tyr	Ala	Ile	Asn	Gly	Gly	Val	Asp	Glu	Lys	Leu	Lys	Met	Gln	
		445					450					455				
gtt	ggc	ccg	aag	tct	gaa	ccg	atc	aaa	ggc	gat	gtc	ctg	aac	tat	gat	1445
Val	Gly	Pro	Lys	Ser	Glu	Pro	Ile	Lys	Gly	Asp	Val	Leu	Asn	Tyr	Asp	
	460					465					470					
gaa	gtg	atg	gag	cgc	atg	gat	cac	ttc	atg	gac	tgg	ctg	gct	aaa	cag	1493
Glu	Val	Met	Glu	Arg	Met	Asp	His	Phe	Met	Asp	Trp	Leu	Ala	Lys	Gln	
475					480					485					490	
tac	atc	act	gca	ctg	aac	atc	atc	cac	tac	atg	cac	gac	aag	tac	agc	1541
Tyr	Ile	Thr	Ala	Leu	Asn	Ile	Ile	His	Tyr	Met	His	Asp	Lys	Tyr	Ser	
				495					500					505		
tac	gaa	gcc	tct	ctg	atg	gcg	ctg	cac	gac	cgt	gac	gtt	atc	cgc	acc	1589
Tyr	Glu	Ala	Ser	Leu	Met	Ala	Leu	His	Asp	Arg	Asp	Val	Ile	Arg	Thr	
			510					515					520			
atg	gcg	tgt	ggc	atc	gct	ggc	ctg	tcc	gtt	gct	gct	gac	tcc	ctg	tct	1637
Met	Ala	Cys	Gly	Ile	Ala	Gly	Leu	Ser	Val	Ala	Ala	Asp	Ser	Leu	Ser	
		525					530					535				

gca atc aaa tat gcg aaa gtt aaa ccg att cgt gac gaa gac ggt ctg Ala Ile Lys Tyr Ala Lys Val Lys Pro Ile Arg Asp Glu Asp Gly Leu 540 545 550	1685
gct atc gac ttc gaa atc gaa ggc gaa tac ccg cag ttt ggt aac aat Ala Ile Asp Phe Glu Ile Glu Gly Glu Tyr Pro Gln Phe Gly Asn Asn 555 560 565 570	1733
gat ccg cgt gta gat gac ctg gct gtt gac ctg gta gaa cgt ttc atg Asp Pro Arg Val Asp Asp Leu Ala Val Asp Leu Val Glu Arg Phe Met 575 580 585	1781
aag aaa att cag aaa ctg cac acc tac cgt gac gct atc ccg act cag Lys Lys Ile Gln Lys Leu His Thr Tyr Arg Asp Ala Ile Pro Thr Gln 590 595 600	1829
tct gtt ctg acc atc act tct aac gtt gtg tat ggt aag aaa acg ggt Ser Val Leu Thr Ile Thr Ser Asn Val Val Tyr Gly Lys Lys Thr Gly 605 610 615	1877
aac acc cca gac ggt cgt cgt gct ggc gcg ccg ttc gga ccg ggt gct Asn Thr Pro Asp Gly Arg Arg Ala Gly Ala Pro Phe Gly Pro Gly Ala 620 625 630	1925
aac ccg atg cac ggt cgt gac cag aaa ggt gca gta gcc tct ctg act Asn Pro Met His Gly Arg Asp Gln Lys Gly Ala Val Ala Ser Leu Thr 635 640 645 650	1973
tcc gtt gct aaa ctg ccg ttt gct tac gct aaa gat ggt atc tcc tac Ser Val Ala Lys Leu Pro Phe Ala Tyr Ala Lys Asp Gly Ile Ser Tyr 655 660 665	2021
acc ttc tct atc gtt ccg aac gca ctg ggt aaa gac gac gaa gtt cgt Thr Phe Ser Ile Val Pro Asn Ala Leu Gly Lys Asp Asp Glu Val Arg 670 675 680	2069
aag acc aac ctg gct ggt ctg atg gat ggt tac ttc cac cac gaa gca Lys Thr Asn Leu Ala Gly Leu Met Asp Gly Tyr Phe His His Glu Ala 685 690 695	2117
tcc atc gaa ggt ggt cag cac ctg aac gtt aac gtg atg aac cgt gaa Ser Ile Glu Gly Gly Gln His Leu Asn Val Asn Val Met Asn Arg Glu 700 705 710	2165
atg ctg ctc gac gcg atg gaa aac ccg gaa aaa tat ccg cag ctg acc Met Leu Leu Asp Ala Met Glu Asn Pro Glu Lys Tyr Pro Gln Leu Thr 715 720 725 730	2213
atc cgt gta tct ggc tac gca gta cgt ttc aac tcg ctg act aaa gaa Ile Arg Val Ser Gly Tyr Ala Val Arg Phe Asn Ser Leu Thr Lys Glu 735 740 745	2261
cag cag cag gac gtt att act cgt acc ttc act caa tct atg taa Gln Gln Gln Asp Val Ile Thr Arg Thr Phe Thr Gln Ser Met 750 755 760	2306
taagctttga ctgaaatcg	2325

<210> 8
 <211> 760
 <212> PRT
 <213> Escherichia coli

<400> 8

Met	Ser	Glu	Leu	Asn	Glu	Lys	Leu	Ala	Thr	Ala	Trp	Glu	Gly	Phe	Thr	1	5	10	15
Lys	Gly	Asp	Trp	Gln	Asn	Glu	Val	Asn	Val	Arg	Asp	Phe	Ile	Gln	Lys	20	25	30	
Asn	Tyr	Thr	Pro	Tyr	Glu	Gly	Asp	Glu	Ser	Phe	Leu	Ala	Gly	Ala	Thr	35	40	45	
Glu	Ala	Thr	Thr	Thr	Leu	Trp	Asp	Lys	Val	Met	Glu	Gly	Val	Lys	Leu	50	55	60	
Glu	Asn	Arg	Thr	His	Ala	Pro	Val	Asp	Phe	Asp	Thr	Ala	Val	Ala	Ser	65	70	75	80
Thr	Ile	Thr	Ser	His	Asp	Ala	Gly	Tyr	Ile	Asn	Lys	Gln	Leu	Glu	Lys	85	90	95	
Ile	Val	Gly	Leu	Gln	Thr	Glu	Ala	Pro	Leu	Lys	Arg	Ala	Leu	Ile	Pro	100	105	110	
Phe	Gly	Gly	Ile	Lys	Met	Ile	Glu	Gly	Ser	Cys	Lys	Ala	Tyr	Asn	Arg	115	120	125	
Glu	Leu	Asp	Pro	Met	Ile	Lys	Lys	Ile	Phe	Thr	Glu	Tyr	Arg	Lys	Thr	130	135	140	
His	Asn	Gln	Gly	Val	Phe	Asp	Val	Tyr	Thr	Pro	Asp	Ile	Leu	Arg	Cys	145	150	155	160
Arg	Lys	Ser	Gly	Val	Leu	Thr	Gly	Leu	Pro	Asp	Ala	Tyr	Gly	Arg	Gly	165	170	175	
Arg	Ile	Ile	Gly	Asp	Tyr	Arg	Arg	Val	Ala	Leu	Tyr	Gly	Ile	Asp	Tyr	180	185	190	
Leu	Met	Lys	Asp	Lys	Leu	Ala	Gln	Phe	Thr	Ser	Leu	Gln	Ala	Asp	Leu	195	200	205	
Glu	Asn	Gly	Val	Asn	Leu	Glu	Gln	Thr	Ile	Arg	Leu	Arg	Glu	Glu	Ile	210	215	220	
Ala	Glu	Gln	His	Arg	Ala	Leu	Gly	Gln	Met	Lys	Glu	Met	Ala	Ala	Lys	225	230	235	240
Tyr	Gly	Tyr	Asp	Ile	Ser	Gly	Pro	Ala	Thr	Asn	Ala	Gln	Glu	Ala	Ile	245	250	255	
Gln	Trp	Thr	Tyr	Phe	Gly	Tyr	Leu	Ala	Ala	Val	Lys	Ser	Gln	Asn	Gly	260	265	270	
Ala	Ala	Met	Ser	Phe	Gly	Arg	Thr	Ser	Thr	Phe	Leu	Asp	Val	Tyr	Ile	275	280	285	
Glu	Arg	Asp	Leu	Lys	Ala	Gly	Lys	Ile	Thr	Glu	Gln	Glu	Ala	Gln	Glu	290	295	300	
Met	Val	Asp	His	Leu	Val	Met	Lys	Leu	Arg	Met	Val	Arg	Phe	Leu	Arg	305	310	315	320
Thr	Pro	Glu	Tyr	Asp	Glu	Leu	Phe	Ser	Gly	Asp	Pro	Ile	Trp	Ala	Thr	325	330	335	
Glu	Ser	Ile	Gly	Gly	Met	Gly	Leu	Asp	Gly	Arg	Thr	Leu	Val	Thr	Lys	340	345	350	

Asn	Ser	Phe	Arg	Phe	Leu	Asn	Thr	Leu	Tyr	Thr	Met	Gly	Pro	Ser	Pro	355	360	365
Glu	Pro	Asn	Met	Thr	Ile	Leu	Trp	Ser	Glu	Lys	Leu	Pro	Leu	Asn	Phe	370	375	380
Lys	Lys	Phe	Ala	Ala	Lys	Val	Ser	Ile	Asp	Thr	Ser	Ser	Leu	Gln	Tyr	385	390	400
Glu	Asn	Asp	Asp	Leu	Met	Arg	Pro	Asp	Phe	Asn	Asn	Asp	Asp	Tyr	Ala	405	410	415
Ile	Ala	Cys	Cys	Val	Ser	Pro	Met	Ile	Val	Gly	Lys	Gln	Met	Gln	Phe	420	425	430
Phe	Gly	Ala	Arg	Ala	Asn	Leu	Ala	Lys	Thr	Met	Leu	Tyr	Ala	Ile	Asn	435	440	445
Gly	Gly	Val	Asp	Glu	Lys	Leu	Lys	Met	Gln	Val	Gly	Pro	Lys	Ser	Glu	450	455	460
Pro	Ile	Lys	Gly	Asp	Val	Leu	Asn	Tyr	Asp	Glu	Val	Met	Glu	Arg	Met	465	470	475
Asp	His	Phe	Met	Asp	Trp	Leu	Ala	Lys	Gln	Tyr	Ile	Thr	Ala	Leu	Asn	485	490	495
Ile	Ile	His	Tyr	Met	His	Asp	Lys	Tyr	Ser	Tyr	Glu	Ala	Ser	Leu	Met	500	505	510
Ala	Leu	His	Asp	Arg	Asp	Val	Ile	Arg	Thr	Met	Ala	Cys	Gly	Ile	Ala	515	520	525
Gly	Leu	Ser	Val	Ala	Ala	Asp	Ser	Leu	Ser	Ala	Ile	Lys	Tyr	Ala	Lys	530	535	540
Val	Lys	Pro	Ile	Arg	Asp	Glu	Asp	Gly	Leu	Ala	Ile	Asp	Phe	Glu	Ile	545	550	555
Glu	Gly	Glu	Tyr	Pro	Gln	Phe	Gly	Asn	Asn	Asp	Pro	Arg	Val	Asp	Asp	565	570	575
Leu	Ala	Val	Asp	Leu	Val	Glu	Arg	Phe	Met	Lys	Lys	Ile	Gln	Lys	Leu	580	585	590
His	Thr	Tyr	Arg	Asp	Ala	Ile	Pro	Thr	Gln	Ser	Val	Leu	Thr	Ile	Thr	595	600	605
Ser	Asn	Val	Val	Tyr	Gly	Lys	Lys	Thr	Gly	Asn	Thr	Pro	Asp	Gly	Arg	610	615	620
Arg	Ala	Gly	Ala	Pro	Phe	Gly	Pro	Gly	Ala	Asn	Pro	Met	His	Gly	Arg	625	630	635
Asp	Gln	Lys	Gly	Ala	Val	Ala	Ser	Leu	Thr	Ser	Val	Ala	Lys	Leu	Pro	645	650	655
Phe	Ala	Tyr	Ala	Lys	Asp	Gly	Ile	Ser	Tyr	Thr	Phe	Ser	Ile	Val	Pro	660	665	670
Asn	Ala	Leu	Gly	Lys	Asp	Asp	Glu	Val	Arg	Lys	Thr	Asn	Leu	Ala	Gly	675	680	685
Leu	Met	Asp	Gly	Tyr	Phe	His	His	Glu	Ala	Ser	Ile	Glu	Gly	Gly	Gln	690	695	700

